

### **Listing of Claims**

This listing of claims replaces all prior versions and listings of claims in the application.

1. (PREVIOUSLY PRESENTED) A method for quantifying the absolute amount of at least two target nucleic acid sequences corresponding to at least two genes in a biological sample, comprising the steps of:
  - a) preparing a sample by combining in a sample the biological sample comprising the at least two target nucleic acid sequences corresponding to the at least two genes and a known amount of at least two standard nucleic acids, wherein said at least two standard nucleic acids have a nucleotide sequence that is one base different than the respective target nucleic acid sequence;
  - b) amplifying the sample of step a);
  - c) using a single base primer extension reaction at the site of differentiation to enhance a mass difference between the at least two standard nucleic acid sequences and the at least two target nucleic acid sequences corresponding to the at least two genes at the site wherein each of the standard nucleic acid sequence differs from the respective target nucleic acid sequence corresponding to the at least two genes resulting in enhanced products with different masses so that the mass differences between the at least two standard and the at least two target nucleic acid sequences corresponding to the at least two genes can be detected;
  - d) detecting the enhanced products using one MALDI-TOF mass spectrometry analysis to obtain a peak area for each enhanced target and standard in one reaction; and
  - e) quantifying the amount of the initial target by measuring a ratio of each peak area resulting from the amplified target nucleic acid and its corresponding amplified standard nucleic acid and then calculating the absolute amount based on the amount of the standard initially added to the sample.

2. (PREVIOUSLY PRESENTED) The method of claim 1, wherein the at least two target nucleic acid sequences corresponding to the at least two genes are from an infectious agent.
3. (PREVIOUSLY PRESENTED) The method of claim 1, wherein the at least two target nucleic acid sequences corresponding to the at least two genes are mRNA transcripts.
- 4-9. (CANCELED)
10. (PREVIOUSLY PRESENTED) The method of claim 1, wherein one measures the absolute amount of at least 5 target nucleic acid sequences corresponding to at least 5 genes using at least 5 respective standard nucleic acids.
11. (PREVIOUSLY PRESENTED) The method of claim 1, wherein one measures the absolute amount of at least 10 target nucleic acid sequences corresponding to at least 10 genes using at least 10 respective standard nucleic acids.
12. (PREVIOUSLY PRESENTED) The method of claim 1, wherein one measures the absolute amount of 25 target nucleic acid sequences corresponding to at least 25 genes using at least 25 respective standard nucleic acids.
13. (PREVIOUSLY PRESENTED) The method of claim 1, wherein one measures the absolute amount of 50 target nucleic acid sequences corresponding to at least 50 genes using at least 50 respective standard nucleic acids.
14. -15. (CANCELED)